



Blast 2 Sequences results

PubMed

Entrez

BLAST

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Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.6 [Apr-09-2003]

EXHIBIT

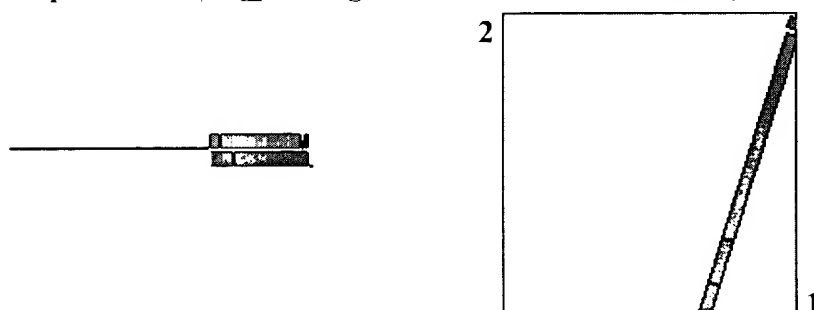
B

Matrix BLOSUM62 gap open: 11 gap extension: 1

x_dropoff: 50 expect: 10.000 wordsize: 3 Filter ☒ Align

Sequence 1 lc|seq_1 Length 1337 (1 .. 1337) - SEQ ID NO:1

Sequence 2 lc|seq_2 Length 437 (1 .. 437) - SEQ ID NO:4



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 540 bits (1392), Expect = e-152

Identities = 288/432 (66%), Positives = 322/432 (73%), Gaps = 13/432 (3%)

```

Query: 914  MYQSRPGPVAVPVQPTRPIKTFQKKNDPKDEALAKLINGVHL-PLSTSPNQGXNXXXXX 972
           MYQSRPGPV VPVQP+RP K F +K DPKDEALAKLING H P SP+ G
Sbjct: 1    MYQSRPGVPVPVQPSRPPKAFRLKIDPKDEALAKLINGAHSSPMLSPSPGKGPAPPAV 60

Query: 973  XXXXXXXXRLEPSLSIQEKQGGLRDLFGXXXXXXXXXXXXXXXXXXXXXLSGEPKTPSVE 1032
           +L PS SI+EKQGGL DLFG L +P T S E
Sbjct: 61   APRPKAPLQLGPSSSIKEKQGGLDLFGQKLPIAHTPPPPAPPLP---LPEDPGTSLAE 117

Query: 1033 SHALTEPMEDKNISTKLLVPSGSVCFSYANAPWKLFLRKEVFYPRENFSPYCLSLLCQQ 1092
           LT+P+ED+ +ST+LL PSGSVCFSY PWKLFLRKEVFYPRENFSPY L LLC+Q
Sbjct: 118  RRCLTQPVEDQGVSTQLLAPSGSVCFSYTGTPWKLFLRKEVFYPRENFSPYYLRLLCEQ 177

Query: 1093 ILRDTFTESCTRISQDERHKMKGLLDLEVSLETLDIVEDSIKKRIVVAARDNWANYFSR 1152
           ILRDTF+ESC RISQ+ER KMK LLG LEV L++L EDS+KKRIVVAARDNWANYFSR
Sbjct: 178  ILRDTFSESCIRISQNERRKMKDLLGGLEVDLDSLTTEDSVKKRIVVAARDNWANYFSR 237

Query: 1153 IFPVSGESGSDVQLLGVSHRGLRLLKVTQSPSFHLDQLKTLCSYSYAEVLTVCGRGSTL 1212
           FFPVSGESGSDVQLL VSHRGLRLLKVTQ P DQLK LCSYS+AEVL V+CRG STL
Sbjct: 238  FFPVSGESGSDVQLLAVSHRGLRLLKVTQGPGLRPDQLKILCSYSFAEVLGVECRGGSTL 297

Query: 1213 ELSLKNEQLILHTAWARAIKAMVDLFLSELKRDGSGYVIALRSYITDDNSLLSFHRGDLIR 1272
           ELSLK+EQL+LHTA ARAI+A+V+LFL+EL+KDSGYVIALRSYITD+ SLLSFHRGDLI+
Sbjct: 298  ELSLKSEQLVLHTARARAIEALVELFLNELKFDGSGYVIALRSYITDNCNSLLSFHRGDLIK 357

Query: 1273 LLPVTALEPGWQFGSAGGRSGLFPDDVVQFAAAPDLSFSLGKPNWQR-----KSK 1323
           LLPV LEPGWQFGSAGGRSGLFP D+VQFAAAPD SFS +R+ W + ++

```



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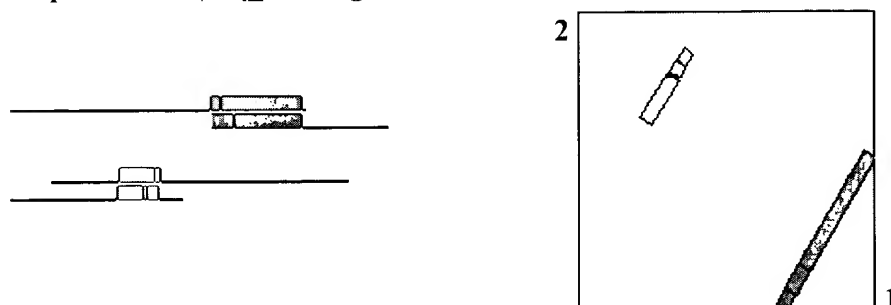
BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.6 [Apr-09-2003]

Matrix BLOSUM62 gap open: 11 gap extension: 1

x_dropoff: 50 expect: 10.000 wordsize: 3 Filter ☒ Align

Sequence 1 lc|seq_1 Length 1337 (1 .. 1337) - SEQ ID NO:1

Sequence 2 lc|seq_2 Length 786 (1 .. 786) - SEQ ID NO:6



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 540 bits (1391), Expect = e-151

Identities = 282/408 (69%), Positives = 314/408 (76%), Gaps = 4/408 (0%)

```

Query: 914 MYQSRPGPVAVPVQPTRPIKTFQKKNDPKDEALAKLINGVHL-PLSTSPNQGXXXXXXX 972
           MYQSRPGPV VPVQP+RP K F +K DPKDEALAKLING H P SP+ G
Sbjct: 1 MYQSRPGVPVPVQPSRPPKAFLRKIDPKDEALAKLINGAHSSPPMLSPSPGKGP PPAV 60

Query: 973 XXXXXXXXRLEPSLSIQEKQGPLRDLFGXXXXXXXXXXXXXXXXXXXXLSGEPKTPSVE 1032
           +L PS SI+EKQGPL DLFG L +P T S E
Sbjct: 61 APRPKAPLQLGPSSSIKEKQGPLLDLFGQKLPIAHTPPPPAPPLP---LPEDPGTLSAE 117

Query: 1033 SHALTEPMEDKNISTKLLVPSGSVCFSYANAPWKFLRKEVFYPRENFSHPYCLSLCQ 1092
           LT+P+ED+ +ST+LL PSGSVCFSY PWKLFLRKEVFYPRENFSHPY L LLC+Q
Sbjct: 118 RRCLTQPVEDQGVSTQLLAPSGSVCFSYTGTPWKFLRKEVFYPRENFSHPYLLRLLCEQ 177

Query: 1093 ILRDTFTESCTRISQDERHKMKGLLDLEVSLETLDIVEDSIKKRIVVAARDNWANYFSR 1152
           ILRDTF+ESC RISQ+ER KMK LLG LEV L++L EDS+KKRIVVAARDNWANYFSR
Sbjct: 178 ILRDTFSESCIRISQNERRKMKDLLGGLEVDLDSLTTTSDSVKKRIVVAARDNWANYFSR 237

Query: 1153 IFPVSGESGSDVQLLGVSHRGLRLLKVTQSPSFHLDQLKTLCSYSYAEVLTVCRCRSTL 1212
           FFPVSGESGSDVQLL VSHRGLRLLKVTQ P DQLK LCSYS+AEVL V+CRG STL
Sbjct: 238 FFPVSGESGSDVQLLAVSHRGLRLLKVTQGPGLRPDQLKILCSYSFAEVLGVECRGGSTL 297

Query: 1213 ELSLKNEQLILHTAWARAIKAMVDLFLSELKDSGYVIALRSYITDDNSLLSFHRGDLIR 1272
           ELSLK+EQL+LHTA ARAI+A+V+LFL+EL+KDSGYVIALRSYITD+ SLLSFHRGDLI+
Sbjct: 298 ELSLKSEQLVLHTARARAIEALVELFLNELKKDSGYVIALRSYITDNC SLLSFHRGDLIK 357

Query: 1273 LLPVTALEPGWQFGSAGGRSGLFPDDVVQPAAAPDLSFSLGKRNSWQR 1320
           LLPV LEPGWQFGSAGGRSGLFP D+VQPAAAPD SFS +R+ W +

```



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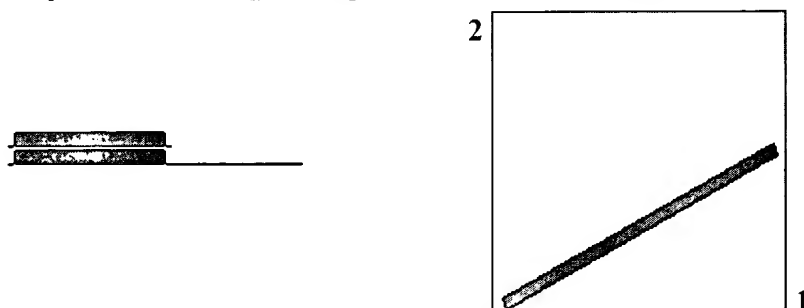
BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.6 [Apr-09-2003]

Matrix BLOSUM62 gap open: 11 gap extension: 1

x_dropoff: 50 expect: 10.000 wordsize: 3 Filter ☒

Sequence 1 lc|seq_1 Length 437 (1 .. 437) - SEQ ID NO: 4

Sequence 2 lc|seq_2 Length 786 (1 .. 786) - SEQ ID NO: 6



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 711 bits (1836), Expect = 0.0

Identities = 365/404 (90%), Positives = 365/404 (90%)

```

Query: 20 KAFLRKIDPKDEALAKLINGXXXXXXXXXXXXXXXXXXXXXXXXXXXXLQLGPSSSIKEK 79
          KAFLRKIDPKDEALAKLING                                     LQLGPSSSIKEK
Sbjct: 20 KAFLRKIDPKDEALAKLINGAHSSPPMLSPSPGKPPPAVAPRPKAPLQLGPSSSIKEK 79

Query: 80 QGPLLDLFGQKLPIAHTXXXXXXXXXXXXXEDPGTLSAERRCLTQPVEDQGVSTQLLAPSG 139
          QGPLLDLFGQKLPIAHT                                     EDPGTLAERRCLTQPVEDQGVSTQLLAPSG
Sbjct: 80 QGPLLDLFGQKLPIAHTPPPPAPPLPLPEDPGTLSAERRCLTQPVEDQGVSTQLLAPSG 139

Query: 140 SVCFSYTGTPWKFLRKEVFYPRENFSPHYLRLLCEQILRDTFSESCIRISQNERRKMK 199
          SVCFSYTGTPWKFLRKEVFYPRENFSPHYLRLLCEQILRDTFSESCIRISQNERRKMK
Sbjct: 140 SVCFSYTGTPWKFLRKEVFYPRENFSPHYLRLLCEQILRDTFSESCIRISQNERRKMK 199

Query: 200 DLLGGLEVLDLSLTTTEDSVKKRIVVAARDNWANYFSRFFPVSGESGSDVQLLAVSHRGL 259
          DLLGGLEVLDLSLTTTEDSVKKRIVVAARDNWANYFSRFFPVSGESGSDVQLLAVSHRGL
Sbjct: 200 DLLGGLEVLDLSLTTTEDSVKKRIVVAARDNWANYFSRFFPVSGESGSDVQLLAVSHRGL 259

Query: 260 RLLKVTQGGLRPDQLKILCSYSFAEVLGVECPGGSTLELSLKSEQLVLHTARAPAIEAL 319
          RLLKVTQGGLRPDQLKILCSYSFAEVLGVECPGGSTLELSLKSEQLVLHTARAPAIEAL
Sbjct: 260 RLLKVTQGGLRPDQLKILCSYSFAEVLGVECPGGSTLELSLKSEQLVLHTARAPAIEAL 319

Query: 320 VELFLNELKKDSGYVIALRSYITDNCSSLFSFHGDLIKLLPVATLEPGWQFGSAGGRSGL 379
          VELFLNELKKDSGYVIALRSYITDNCSSLFSFHGDLIKLLPVATLEPGWQFGSAGGRSGL
Sbjct: 320 VELFLNELKKDSGYVIALRSYITDNCSSLFSFHGDLIKLLPVATLEPGWQFGSAGGRSGL 379

Query: 380 FPADIVQPAAPDFSFSKEQSRSGWHKGQLSNGEPGLARWDRASE 423
          FPADIVQPAAPDFSFSKEQSRSGWHKGQLSNGEPGLARWDRASE

```



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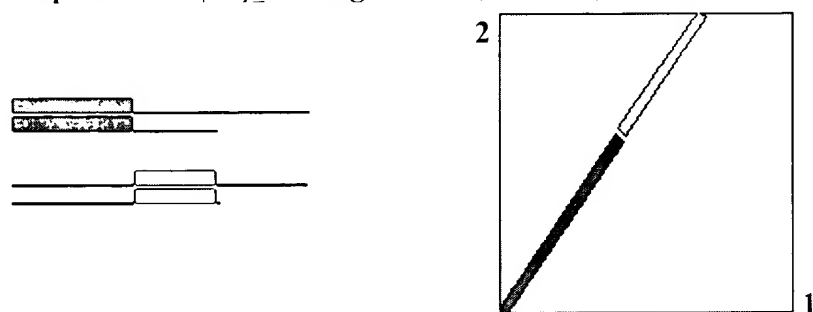
BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.6 [Apr-09-2003]

Match: 1 Mismatch: -2 gap open: 5 gap extension: 2

x_dropoff: 50 expect: 10.000¹ wordsize: 11 Filter ☒

Sequence 1 lcl|seq_1 Length 6293 (1 .. 6293) - SEQ ID NO: 2

Sequence 2 lcl|seq_2 Length 4375 (1 .. 4375) - SEQ ID NO: 3



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 4936 bits (2567), Expect = 0.0

Identities = 2567/2567 (100%)

Strand = Plus / Plus



Query: 1 cgctgggactgtcacctaccaggtgcacaagttcataaacagaaacaggggccacctgga 60

Sbjct: 1 cgctgggactgtcacctaccaggtgcacaagttcataaacagaaacaggggccacctgga 60

Query: 61 ccccgctgtgctggagatgctcaggcagagccagctgcaggtgacctagccttcctttca 120

Sbjct: 61 ccccgctgtgctggagatgctcaggcagagccagctgcaggtgacctagccttcctttca 120

Query: 121 gctcatgggcagcctgttccaagaagcagagccccaggtgggactgagcaaaacaaacc 180

Sbjct: 121 gctcatgggcagcctgttccaagaagcagagccccaggtgggactgagcaaaacaaacc 180

Query: 181 cacattggcctctcgattccagcagaccctgggtgacttgctagctcggctaggcagcag 240

Sbjct: 181 cacattggcctctcgattccagcagaccctgggtgacttgctagctcggctaggcagcag 240



Blast 2 Sequences results

PubMed

Entrez

BLAST

GMM

Taxonomy

Structure

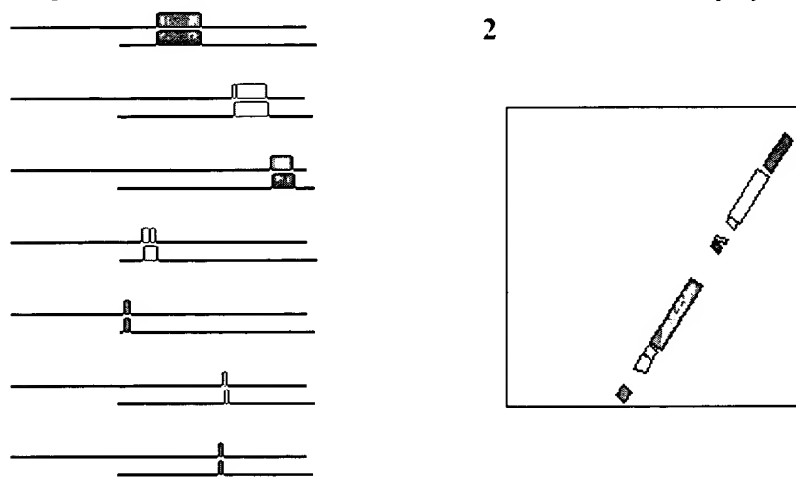
BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.6 [Apr-09-2003]

Match: 1 Mismatch: -2 gap open: 5 gap extension: 2

x_dropoff: 50 expect: 10.000 wordsize: 11 Filter ☒

Sequence 1 lcl|seq_1 Length 6293 (1 .. 6293) - SEQ ID NO: 2

Sequence 2 lcl|seq_2 Length 4174 (1 .. 4174) - SEQ ID NO: 5



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 771 bits (401), Expect = 0.0

Identities = 735/902 (81%)

Strand = Plus / Plus

```

Query: 3156 caccgccgctccaccagcactccaccgcctctgtctggggagcccaagacccttcag 3215
          ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
Sbjct: 847  caccgccacctccaccagcgcaccactgcctctgcccagaggaccagggacccttcag 906

```

```

Query: 3216 tggagtctcatgccttgacagagcccatggaggacaagaacatctccacaaagctccttg 3275
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 907  cagagcgtcgttgcttgacacagcccgaggaggaccaggggtctccaccagctactcg 966

```

```

Query: 3276 tgccctctggaagtgtgtgcttctcctatgccaatgcaccctggaagttgttcttacgca 3335
          ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 967  cgccctctggcagcgtgtgcttctcctacaccggcacgcctggaagttgttcttacgca 1026

```



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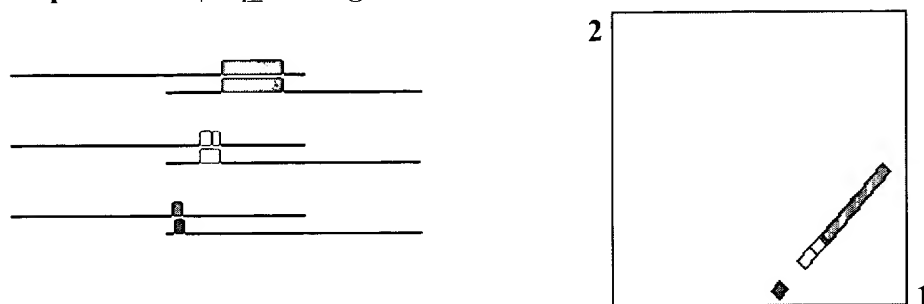
BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.6 [Apr-09-2003]

Match: 1 Mismatch: -2 gap open: 5 gap extension: 2

x_dropoff: 50 expect: 10.000 wordsize: 11 Filter ☒

Sequence 1 lc|seq_1 Length 4375 (1 .. 4375) - SEQ ID NO: 3

Sequence 2 lc|seq_2 Length 3780 (1 .. 3780) - SEQ ID NO: 5



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 771 bits (401), Expect = 0.0

Identities = 735/902 (81%)

Strand = Plus / Plus

```

Query: 3156 cccccccgctccaccagcactcccaccgctctgtctggggagcccaagacccttcag 3215
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 847  cccccccacctccaccagcgccaccactgcctctgcccaggagaccaggacccttcag 906
  
```

```

Query: 3216 tggagtctcatgccttgacagagcccatggaggacaagaacatctccaaaagctccttg 3275
          ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 907  cagagcgctgcttgcttgacacagcccgaggaggaccaggggtctccaccagctactcg 966
  
```

```

Query: 3276 tgccctctggaagtgtgtgcttctcctatgccaatgcaccctggaagttgttcttacgca 3335
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 967  cgccctctggcagcggtgtgcttctcctacaccggcagccctggaagttgttcttacgca 1026
  
```

```

Query: 3336 aggaggtgttctacccccgggagaacttcagtcattccatactgcctcagtcctctgcc 3395
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 1027 aggaggtgttctacccacgggagaacttcagccattccctactacctgaggctcctctgtg 1086
  
```



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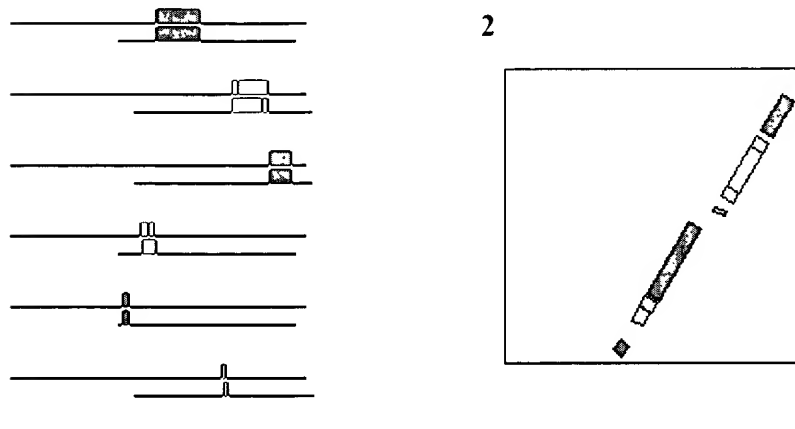
BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.6 [Apr-09-2003]

Match: 1 Mismatch: -2 gap open: 5 gap extension: 2

x_dropoff: 50 expect: 10.000 wordsize: 11 Filter ☒ Align

Sequence 1 lc|seq_1 Length 6293 (1 .. 6293) - SEQ ID NO: 2

Sequence 2 lc|seq_2 Length 3780 (1 .. 3780) - SEQ ID NO: 7



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 771 bits (401), Expect = 0.0

Identities = 735/902 (81%)

Strand = Plus / Plus



Query: 3156 cccccgcctccaccagcactcccaccgcctctgtctggggagcccaagacccttcag 3215

Sbjct: 847 cccccacctccaccagcgccaccactgcctctgcccaggaccaggaccccttcag 906

Query: 3216 tggagtctcatgccttgacagagcccatggaggacaagaacatctccacaaagctccttg 3275

Sbjct: 907 cagagcgtcgttgcttgacacagcccgtggaggaccaggggtctccaccagctactcg 966

Query: 3276 tgccctctggaagtgtgtgcttctcctatgccaatgcaccctggaagttgttcttacgca 3335

Sbjct: 967 cgccctctggcagcgtgtgtgcttctcctacaccggcacgcctggaagttgttcttacgca 1026

Query: 3336 aggaggtgttctacccccgggagaacttcagtcacatactgcctcagtcctccttgcc 3395



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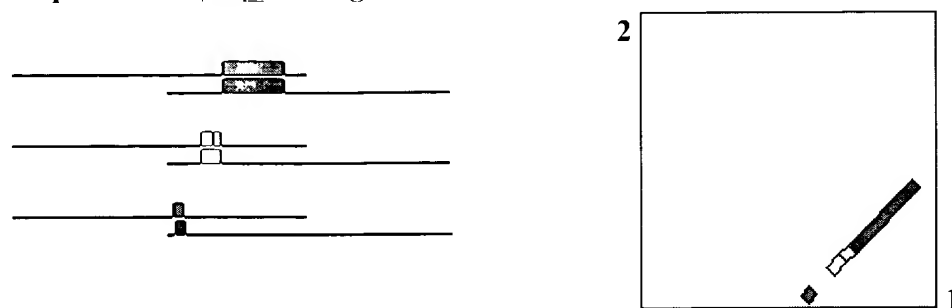
BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.6 [Apr-09-2003]

Match: 1 Mismatch: -2 gap open: 5 gap extension: 2

x dropoff: 50 expect: 10.000i wordsize: 11 Filter  Align

Sequence 1 lcl|seq_1 Length 4375 (1 .. 4375) - SEQ ID NO: 3

Sequence 2 |cl|seq_2 Length 4174 (1 .. 4174) - SEQ ID NO:7



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 771 bits (401), Expect = 0.0

Identities = 735/902 (81%)

Strand = Plus / Plus



```
Query: 3156 cccccgcctccaccagcactcccaccgcctctgtctggggagcccaagacccttcag 3215
          ||||||| ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 847 cccccacctccaccagcgcaccactgcctctgccgaggaccacaggacccttcag 906
```

Query: 3216 tggagtctcatgccttgacagagcccatggaggacaagaacatctccacaaagctccttg 3275
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 907 cagagcqtctgttgccttgacacagcccgtggaggaccagggggtctccaccagctactcg 966

Query: 3276 tggccctctggaagtgtgtgcttctcctatgccaatgcacctggaagttgttcttacgca 3335
 |||||
 Sbjct: 967 cggccctctggcagcgtgtgcttctcctacacggcgacggcctggaagttgttcttacgca 1026

Query: 3336 aggaggtgttctacccccgggagaacttcagtcatccatactgcctcagtcctctctgcc 3395
 |||
 Sbjct: 1027 aggaggtgttctacccacgggagaacttcagccatccctactacctgaggtcctctgtg 1086



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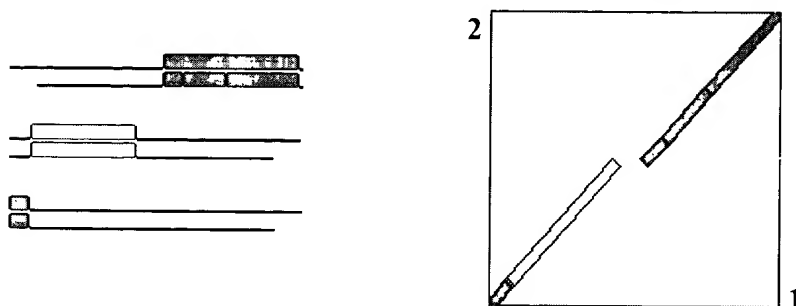
BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.6 [Apr-09-2003]

Match: 1 Mismatch: -2 gap open: 5 gap extension: 2

x_dropoff: 50 expect: 10.0001 wordsize: 11 Filter ☒ Align

Sequence 1 lc|seq_1 Length 4174 (1 .. 4174) - SEQ ID NO: 5

Sequence 2 lc|seq_2 Length 3780 (1 .. 3780) - SEQ ID NO: 7



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 3673 bits (1910), Expect = 0.0
Identities = 1924/1926 (99%), Gaps = 2/1926 (0%)
Strand = Plus / Plus

```
Query: 2222 agcgccctgcccacccttggagccaggcacacagtgacgactcggaggccaccagcctgt 2281
          |||
Sbjct: 1828 agcgccctgcccacccttggagccaggcacacagtgacgactcggaggccaccagcctgt 1887
```

```
Query: 2282 cctctgtggcctatgcctttctgcccgaactcccacagctacaccatgcaggaattcgccc 2341
          |||
Sbjct: 1888 cctctgtggcctatgcctttctgcccgaactcccacagctacaccatgcaggaattcgccc 1947
```

```
Query: 2342 ggcgttacttccggagggtcccaggccttgctgggccagactgatggagggtgccgcaggaa 2401
          |||
Sbjct: 1948 ggcgttacttccggagggtcccaggccttgctgggccagactgatggagggtgccgcaggaa 2007
```

```
Query: 2402 aggacacggacagcctggtgcagtacaccaaggctcccatccaggagtcgctcctcagcc 2461
          |||
Sbjct: 2008 aggacacggacagcctggtgcagtacaccaaggctcccatccaggagtcgctcctcagcc 2067
```